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0206-1-9

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/550,163
DATE: 05/04/2000
TIME: 15:28:48

Input Set : A:\2323-150.app
Output Set: N:\CRF3\05042000\I550163.raw

PS

3 <110> APPLICANT: Abbott, Geoffrey W.
4 Sesti, Federico
5 Splawski, Igor
6 Keating, Mark T.
7 Goldstein, Steve A.N.
8 University of Utah Research Foundation
9 Yale University
11 <120> TITLE OF INVENTION: MinK-Related Genes, Formation of Potassium Channels and
12 Association with Cardiac Arrhythmia
14 <130> FILE REFERENCE: KCNE2 et al.
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/550,163
C--> 17 <141> CURRENT FILING DATE: 2000-04-14
19 <150> PRIOR APPLICATION NUMBER: US 60/129,404
20 <151> PRIOR FILING DATE: 1999-04-15
22 <160> NUMBER OF SEQ ID NOS: 20
24 <170> SOFTWARE: PatentIn Ver. 2.0
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27 <211> LENGTH: 732
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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33 <222> LOCATION: (74)..(442)
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38 gcaggaggga agc atg tct act tta tcc aat ttc aca cag acg ctg gaa 109
39 Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu
40 1 5 10
42 gac gtc ttc cga agg att ttt att act tat atg gac aat tgg cgc cag 157
43 Asp Val Phe Arg Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln
44 15 20 25
46 aac aca aca gct gag caa gag gcc ctc caa gcc aaa gtt gat gct gag 205
47 Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu
48 30 35 40
50 aac ttc tac tat gtc atc ctg tac ctc atg gtg atg att gga atg ttc 253
51 Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe
52 45 50 55 60
54 tct ttc atc atc gtg gcc atc ctg gtg agc act gtg aaa tcc aag aga 301
55 Ser Phe Ile Ile Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg
56 65 70 75
58 cgg gaa cac tcc aat gac ccc tac cac cag tac att gta gag gac tgg 349
59 Arg Glu His Ser Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp
60 80 85 90
62 cag gaa aag tac aag agc caa atc ttg aat cta gaa gaa tcg aag gcc 397
63 Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala
64 95 100 105
66 acc atc cat gag aac att ggt gcg gct ggg ttc aaa atg tcc ccc 442

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67 Thr Ile His Glu Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro
68      110      115      120
70 tgataaggga gaaaggcacc aagctaacat ctgacgtcca gacatgaaga gatgccagtg 502
72 ccacgaggca aatccaaatt gtctttgctt agaagaaagt gagttccttg ctctttgttg 562
74 agaattttca tggagattat gtggttggcc aataaagata gatgacattt caatctcagt 622
76 gatttatgct tgcctgttgg agcaatatatt tgtgctgaag acctctttta ctttcggggc 682
78 aagtgaatgt cattttaatc aatatcaatg atgaaaaata agccaaattt      732
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82 <211> LENGTH: 123
83 <212> TYPE: PRT
84 <213> ORGANISM: Homo sapiens
86 <400> SEQUENCE: 2
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88      1      5      10      15
90 Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln Asn Thr Thr Ala
91      20      25      30
93 Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu Asn Phe Tyr Tyr
94      35      40      45
96 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile
97      50      55      60
99 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
100     65      70      75      80
102 Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr
103      85      90      95
105 Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala Thr Ile His Glu
106     100     105     110
108 Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro
109     115     120
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 468
114 <212> TYPE: DNA
115 <213> ORGANISM: Rattus norvegicus
117 <220> FEATURE:
118 <221> NAME/KEY: CDS
119 <222> LOCATION: (35)..(403)
121 <400> SEQUENCE: 3
122 cctgtgagga atctctcatc ctcaaggggg aaac atg acc act tta gcc aac ttg 55
123      Met Thr Thr Leu Ala Asn Leu
124      1      5
126 acg cag acc ctg gag gat gcc ttc aaa aag gtt ttc att act tat atg 103
127 Thr Gln Thr Leu Glu Asp Ala Phe Lys Lys Val Phe Ile Thr Tyr Met
128      10      15      20
130 gac agc tgg agg agg aac aca aca gcc gaa caa cag gcg ctc cag gcc 151
131 Asp Ser Trp Arg Arg Asn Thr Thr Ala Glu Gln Gln Ala Leu Gln Ala
132      25      30      35
134 aga gtg gat gcc gag aac ttc tac tac gtc atc ctg tac ctc atg gtg 199
135 Arg Val Asp Ala Glu Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val
136      40      45      50      55
138 atg atc ggc atg ttc gcc ttc atc gtg gtg gcc atc ctg gtg agc acg 247

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139 Met Ile Gly Met Phe Ala Phe Ile Val Val Ala Ile Leu Val Ser Thr
140      60      65      70
142 gtg aag tgc aag cgg cgg gag cac tcc cag gac ccg tac cac cag tac 295
143 Val Lys Ser Lys Arg Arg Glu His Ser Gln Asp Pro Tyr His Gln Tyr
144      75      80      85
146 atc gtg gag gat tgg cag cag aag tat agg agt cag atc ttg cat ctg 343
147 Ile Val Glu Asp Trp Gln Gln Lys Tyr Arg Ser Gln Ile Leu His Leu
148      90      95      100
150 gaa gac tcc aag gcc acc atc cat gag aac ctg ggg gcg acg ggg ttc 391
151 Glu Asp Ser Lys Ala Thr Ile His Glu Asn Leu Gly Ala Thr Gly Phe
152      105      110      115
154 aca gtg tca ccc tgataaagaa cyagagtcca tctgccccagg aaggggtgct 443
155 Thr Val Ser Pro
156 120
158 tctgccgcct tgaagcccca ctgac 468
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 123
163 <212> TYPE: PRT
164 <213> ORGANISM: Rattus norvegicus
166 <400> SEQUENCE: 4
167 Met Thr Thr Leu Ala Asn Leu Thr Gln Thr Leu Glu Asp Ala Phe Lys
168      1      5      10      15
170 Lys Val Phe Ile Thr Tyr Met Asp Ser Trp Arg Arg Asn Thr Thr Ala
171      20      25      30
173 Glu Gln Gln Ala Leu Gln Ala Arg Val Asp Ala Glu Asn Phe Tyr Tyr
174      35      40      45
176 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ala Phe Ile Val
177      50      55      60
179 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
180      65      70      75      80
182 Gln Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Gln Lys Tyr
183      85      90      95
185 Arg Ser Gln Ile Leu His Leu Glu Asp Ser Lys Ala Thr Ile His Glu
186      100      105      110
188 Asn Leu Gly Ala Thr Gly Phe Thr Val Ser Pro
189      115      120
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 492
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (93)..(401)
201 <400> SEQUENCE: 5
202 aaagggaactc ctgaaactg attgagagcc cagtggtatt gccagcagtt tgagcttcta 60
204 ccgagtcttc cccacctca atccctgttg ct atg gag act acc aat gga acg 113
205      Met Glu Thr Thr Asn Gly Thr
206      1      5
208 gag acc tgg tat gag agc ctg cat gcc gtg ctg aag gct cta aat gcc 161

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209 Glu Thr Trp Tyr Glu Ser Leu His Ala Val Leu Lys Ala Leu Asn Ala
210      10      15      20
212 act ctt cac agc aat ttg ctc tgc cgg cca ggg cca ggg ctg ggg cca 209
213 Thr Leu His Ser Asn Leu Leu Cys Arg Pro Gly Pro Gly Leu Gly Pro
214      25      30      35
216 gac aac cag act gaa gag agg cgg gcc agc cta cct ggc cgt gat gac 257
217 Asp Asn Gln Thr Glu Glu Arg Arg Ala Ser Leu Pro Gly Arg Asp Asp
218      40      45      50      55
220 aac tcc tac atg tac att ctc ttt gtc atg ttt cta ttt gct gta act 305
221 Asn Ser Tyr Met Tyr Ile Leu Phe Val Met Phe Leu Phe Ala Val Thr
222      60      65      70
224 gtg ggc agc ctc atc ctg gga tac acc cgc tcc cgc aaa gtg gac aag 353
225 Val Gly Ser Leu Ile Leu Gly Tyr Thr Arg Ser Arg Lys Val Asp Lys
226      75      80      85
228 cgt agt gac ccc tat cat gtg tat atc aag aac cgt gtg tct atg atc 401
229 Arg Ser Asp Pro Tyr His Val Tyr Ile Lys Asn Arg Val Ser Met Ile
230      90      95      100
232 taacacgaga gggctgggac ggtggaagac caagacacct ggggattgcg tctggggcct 461
234 ccagaactct gctgtggact gcatcaggtc t 492
237 <210> SEQ ID NO: 6
238 <211> LENGTH: 103
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
242 <400> SEQUENCE: 6
243 Met Glu Thr Thr Asn Gly Thr Glu Thr Trp Tyr Glu Ser Leu His Ala
244      1      5      10      15
246 Val Leu Lys Ala Leu Asn Ala Thr Leu His Ser Asn Leu Leu Cys Arg
247      20      25      30
249 Pro Gly Pro Gly Leu Gly Pro Asp Asn Gln Thr Glu Glu Arg Arg Ala
250      35      40      45
252 Ser Leu Pro Gly Arg Asp Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
253      50      55      60
255 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
256      65      70      75      80
258 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile
259      85      90      95
261 Lys Asn Arg Val Ser Met Ile
262      100
265 <210> SEQ ID NO: 7
266 <211> LENGTH: 972
267 <212> TYPE: DNA
268 <213> ORGANISM: Mus musculus
270 <220> FEATURE:
271 <221> NAME/KEY: CDS
272 <222> LOCATION: (241)..(549)
274 <400> SEQUENCE: 7
275 atcctggaaa ctggataatc aatgactctc taggagttgg aaatccgggg actcaaggaa 60
277 gagaaacaaa acaccagtgt ttctgtctgt gcccatittg aaccaagaga tgcaccttgc 120
279 aaggaaactga ggggttgttg gacatccacg aagagatctc caaagatgtc tcagagccag 180

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281 cagagtctct gaactgtttg atcacattcc agctcttccc atacctcaat atctgttgct 240
283 atg gag act tcc aac ggg act gag acc tgg tac atg agc ctc cat gct 288
284 Met Glu Thr Ser Ser Asn Gly Thr Glu Thr Trp Tyr Met Ser Leu His Ala
285 1 5 10 15
287 gtg ctg aag gct ctg aac aca acc ctt cac agt cac ttg ctc tgc cgg 336
288 Val Leu Lys Ala Leu Asn Thr Thr Leu His Ser His Leu Leu Cys Arg
289 20 25 30
291 cct ggg cca gga cca ggg cca gac aat caa act gag gat cgt cgg gct 384
292 Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala
293 35 40 45
295 agc ctt cct ggt cgt aat gac aac tcc tac atg tat att ctc ttt gtc 432
296 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
297 50 55 60
299 atg ttc cta ttt gcc gtc act gtg ggc agt ctc atc ctg gga tat acc 480
300 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
301 65 70 75 80
303 cgt tca cgc aaa gtg gac aaa cgt agt gac ccc tat cat gtg tac atc 528
304 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile
305 85 90 95
307 aag aac cgt gtg tct atg atc tgaatgtgagg aacctgaaga caatggaaga 579
308 Lys Asn Arg Val Ser Met Ile
309 100
311 ttacaatgtc tgaggattgt cttctgggtgc ctccggaact caactcaacc atatcaagcc 639
313 acagtgtatc tatgtaagat caacaggaaa ctggtgaagag gattaggtca ttattaggac 699
315 cagagaagag ggaactgatag gcccagtctt gtggatgaga catttttcga gacacagatg 759
317 cgcattataa actcagagcc catgaacaca tatatataaa gtatggacaa ccagcaagta 819
319 gaagaggaag ctgtgcygaa gggaaatggg gcagaaaagat gctctggata tataatcttt 879
321 taatgtatga tcttcaacat gaaaaacctt gataaaactg agaatgctac ttaaaaaaaa 939
323 aaaaaaaaaa aaaaaaatatt ccgcggccgc aag 972
326 <210> SEQ ID NO: 8
327 <211> LENGTH: 103
328 <212> TYPE: PRT
329 <213> ORGANISM: Mus musculus
331 <400> SEQUENCE: 8
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333 1 5 10 15
335 Val Leu Lys Ala Leu Asn Thr Thr Leu His Ser His Leu Leu Cys Arg
336 20 25 30
338 Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala
339 35 40 45
341 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
342 50 55 60
344 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
345 65 70 75 80
347 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile
348 85 90 95
350 Lys Asn Arg Val Ser Met Ile
351 100
354 <210> SEQ ID NO: 9

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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L:16 M:270 C: Current Application Number differs, Replaced Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20